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model {
### Model for ipd ###
for(i in 1:n.subjects.ipd) {
  #likelihood
  y.ipd[i] ~ dnorm(theta[i], prec.ipd[study.ipd[i]])
  #model
  theta[i] <- mu.ipd[study.ipd[i]] +      b_basey[study.ipd[i]] *
  basey.ipd[i] +
  b_age.ipd[study.ipd[i]]*age.ipd[i]*mod1+b_bmi.ipd[study.ipd[i]]*bmi.
  ipd[i]*mod2 +
  (delta[index.ipd[i]] +
(b_tx_age*age.ipd[i]*mod1+b_tx_bmi*bmi.ipd[i]*mod2)*
  equals(baseline.ipd[i],1))*(1 -equals(treat.ipd[i],baseline.ipd[i]))

  #residual deviance
  dev.ipd[i]<- (y.ipd[i] - theta[i]) * (y.ipd[i] - theta[i])

  #impute missing data
  age.ipd[i]~dnorm(mu.age.ipd,p.age.ipd)
  bmi.ipd[i]~dnorm(mu.bmi.ipd,p.bmi.ipd)
}

for(l in 1:(n.arms.ipd)) {
  #consistency model
  delta[l]~dnorm(md[l], prec.re.ipd[l])
  md[l]<- d[treat.ipd.sum[l]] - d[baseline.ipd.sum[l]] + sw.ipd[l]
  prec.re.ipd[l]<- prec.re * 2 * (m.ipd.sum[l] - 1)/m.ipd.sum[l]

  #residual deviance
  resdev.ipd[l]<- sum(dev.ipd[start.ipd.sum[l]:end.ipd.sum[l]]) *
prec.ipd[study.ipd.sum[l]]
}

#multi-arm adjustment for up to 4 arm studies
sw.ipd[1]<-0
sw.ipd[2]<-0
for (l in 3:n.arms.ipd) {
  sw.ipd[l]<- ((delta[l - 1] - d[treat.ipd.sum[l - 1]] +
d[baseline.ipd.sum[l - 1]]) *
(equals(m.ipd.sum[l],3)+equals(m.ipd.sum[l],4)) +
(delta[l - 2] - d[treat.ipd.sum[l - 2]] + d[baseline.ipd.sum[l -
2]]) * equals(m.ipd.sum[l],4))/ (m.ipd.sum[l]-1)
}

#priors for missing data imputation parameters
mu.age.ipd~dunif(-50,50)
sd.age.ipd~dunif(0,30)
p.age.ipd<-1/pow(sd.age.ipd,2)
mu.bmi.ipd~dunif(-40,40)

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sd.bmi.ipd~dunif(0,20)
p.bmi.ipd<-1/pow(sd.bmi.ipd,2)

for(j in 1:n.trials.ipd) {
  #random effect on baseline outcome coefficient
  b_basey[j]~dnorm(b_basey_mean,prec_basey)
  #prior on covariate main effect coefficients, study-specific
baseline term, outcome se
  b_age.ipd[j]~dnorm(0,1.0E-4)
  b_bmi.ipd[j]~dnorm(0,1.0E-4)
  mu.ipd[j]~dnorm(0,1.0E-4)
  se.ipd[j]~dunif(0,2)
  var.ipd[j]<-se.ipd[j]*se.ipd[j]
  prec.ipd[j]<-1/var.ipd[j]
}

### Model for aggregate data ###
  #impute standard deviation and remove feedback
  sdev.imp~dgamma(alpha,beta)
  sdev.imp.cut<-cut(sdev.imp)
  #parameter to adjust for baseline imbalance, remove feedback
  b_basey_new~dnorm(b_basey_mean,prec_basey)
  ancova.cut<-cut(b_basey_new)

for (j in 1:n.arms.ad) {
  #standard deviation imputed for study arm
  sdev[j]<- sd.y.ad[j]*(1>equals(sd.y.ad[j],0)) +
sdev.imp.cut*equals(sd.y.ad[j],0)
  se[j]<-sdev[j]/sqrt(n.ad[j])
  prec.ad[j]<-1/(se[j]*se[j])

  #likelihood
  y.ad[j] ~ dnorm(theta.ad[j], prec.ad[j])

  #model
  theta.ad[j] <- mu.ad[study.ad[j]] +
    (delta[j + n.arms.ipd]+ancova.cut*imb.ad[j] +
    (b_tx_age*age.ad[study.ad[j]]*mod1 +
    b_tx_bmi*bmi.ad[study.ad[j]]*mod2)*
    (equals(baseline.ad[j],1))) *(1-
    equals(treat.ad[j],baseline.ad[j]))

  #consistency model
  delta[j + n.arms.ipd] ~ dnorm(md.ad[j], prec.re.ad[j])
  md.ad[j]<- d[treat.ad[j]] - d[baseline.ad[j]] + sw.ad[j]
  prec.re.ad[j]<- prec.re * 2 * (m.ad[j] - 1)/m.ad[j]

  #residual deviance

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    resdev.ad[j] <- ((y.ad[j] - theta.ad[j]) * (y.ad[j] - theta.ad[j]) *
prec.ad[j])
}

#multi-arm adjustment for up to 5 arm studies
sw.ad[1]<-0
sw.ad[2]<-0
for (i in 3:3) {
  sw.ad[i]<- ((delta[(i+n.arms.ipd) -1] - d[treat.ad[i-1]] +
d[baseline.ad[i - 1]]) * (equals(m.ad[i],3)+equals(m.ad[i],4)) +
(delta[(i + n.arms.ipd) - 2] - d[treat.ad[i - 2]] + d[baseline.ad[i
- 2]]) * (equals(m.ad[i],4))) / (m.ad[i]-1)
}

for (i in 4:n.arms.ad) {
  sw.ad[i]<- ((delta[(i + n.arms.ipd) - 1] - d[treat.ad[i - 1]] +
d[baseline.ad[i - 1]]) *
(equals(m.ad[i],3)+equals(m.ad[i],4)+equals(m.ad[i],5)) +
(delta[(i + n.arms.ipd) - 2] - d[treat.ad[i - 2]] + d[baseline.ad[i
- 2]]) * (equals(m.ad[i],4)+equals(m.ad[i],5)))+(delta[(i +
n.arms.ipd) - 3] - d[treat.ad[i - 3]] + d[baseline.ad[i - 3]]) *
(equals(m.ad[i],5))) / (m.ad[i]-1)
}

#priors for missing data imputation parameters
mu.age.ad~dunif(-50,50)
sd.age.ad~dunif(0,30)
p.age.ad<-1/pow(sd.age.ad,2)
mu.bmi.ad~dunif(-40,40)
sd.bmi.ad~dunif(0,20)
p.bmi.ad<-1/pow(sd.bmi.ad,2)

for(j in 1:n.trials.ad) {
  #prior on study-specific baseline term
  mu.ad[j]~dnorm(0,1.0E-4)
  #impute missing data
  age.ad[j]~dnorm(mu.age.ad,p.age.ad)
  bmi.ad[j]~dnorm(mu.bmi.ad,p.bmi.ad)
}

#sum of residual deviance for aggregate and individual patient data
totresdev.ad<- sum(resdev.ad[])
totresdev.ipd<- sum(resdev.ipd[])

###Priors for shared parameters###
#priors on treatment effects
d[1]<-0
for (k in 2:n.treatments) {

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    d[k] ~ dnorm(0,1.0E-3)
}

#prior on random treatment effect
tau~ dunif(0,2)
tau.sq <- tau *
prec.re<- 1 / tau.sq

#prior on mean and random effect variance for coefficient on
baseline outcome
b_basey_mean~dnorm(0,1.0E-6)
tau_basey~dunif(0,2)
tau_basey.sq<-tau_basey*tau_basey
prec_basey<-1 / tau_basey.sq

#prior on covariate-treatment interaction coefficients
b_tx_age~dnorm(0,1.0E-4)
b_tx_bmi~dnorm(0,1.0E-4)

###Additional statistical summaries
# pairwise comparisons
for (c in 1: n.treatments) {
  for (k in 1: n.treatments) {
    ef[c,k] <- d[c] - d[k]
  }
}

# ranking and prob{treatment k is the best}
for (k in 1: n.treatments) {
  rk[k]<- n.treatments + 1 - rank(d[,k])
  best[k]<- equals(rk[k],1)
}
}

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